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Applicants: Ashkenazi et al. Attorney's Docket No: 39780-2630P1C74
Serial No: 10/020,445 Group Art Unit: 1647
Filed: October 24, 2001 Examiner: Seharaseyon, Jegatheesan
For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS
ENCODING THE SAME**

Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

DECLARATION OF AUDREY GODDARD, Ph.D.,
PAUL J. GODOWSKI, Ph.D., AUSTIN GURNEY, Ph.D.,
MARGARET ROY and WILLIAM I. WOOD, Ph.D.
UNDER 37 CFR 1.131

We, Audrey Goddard, Ph.D., Paul J. Godowski, Ph.D., Austin Gurney, Ph.D., Margaret Roy and William I. Wood, Ph.D. do hereby declare and say as follows:

1. We are the inventors of the above-identified application.
2. We have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by Kedra *et al.*, "Homo Sapiens mRNA for Synaptogyrin 2," Accession No. AJ002308, published on March 3, 1998.
3. We conceived and reduced to practice the polypeptide designated as PRO615 (SEQ ID NO:162) encoded by the nucleic acid sequences claimed in the above-identified application in the United States prior to March 3, 1998.
4. At the time the PRO615 polypeptide was cloned and sequenced, one of the inventors, Austin Gurney, was responsible for overseeing the cloning of cDNAs which encoded novel polypeptides, including the cDNA claimed in the above-identified application that encoded the PRO615 polypeptide (SEQ ID NO: 162).
5. At the time the PRO615 polypeptide was cloned and sequenced, one of the inventors, Audrey Goddard, was, as still is, responsible for overseeing the sequencing of novel

polypeptides, including the PRO615 polypeptide (SEQ ID NO:162) encoded by the nucleic acid sequences claimed in the above-identified application.

6. At the time the PRO615 polypeptide was cloned and sequenced, one of the inventors, William I. Wood, was, as still is, responsible for overseeing the homology searches for the novel polypeptides, including that for the PRO615 polypeptide (SEQ ID NO:162) encoded by the cDNA claimed in the above-identified application.
7. A cDNA clone, referred to as DNA48304-1323 in the above-identified application, was identified as encoding the PRO615 polypeptide.
8. The full length of the cDNA clone is shown in Figure 60 of the above-identified application. The full-length cDNA sequence has 1512 nucleotide residues. The full length of the PRO615 peptide encoded by DNA46804-1323 is shown in Figure 61 of the above-identified application. The full-length PRO615 polypeptide has 224 amino acid residues, and is homologous to human synaptogyrin.
9. Copies of the pages from the GSeqEdit database which report the cloning, sequencing and functional data for the PRO615 polypeptide sequence, including its homology to human synaptogyrin, as well as the cloning, sequencing data for the nucleic acid sequence encoding PRO615 are attached to this declaration (with the dates redacted) as Exhibit A.
10. The GSeqEdit report shows the full-length nucleic acid sequence for DNA48304-1323 (identified as "DNA48304") and the full-length PRO615 polypeptide encoded by DNA48304. Both the DNA48304 and the PRO615 polypeptide sequences and the homology of PRO615 to human synaptogyrin were obtained prior to March 3, 1998.
11. The DNA48304 sequence shown in the GSeqEdit report is identical to that of SEQ ID NO:161 disclosed in the above-identified application.
12. The beginning of the cDNA sequence corresponding to SEQ ID NO:161 in the above-identified application is shown on page 1 of the GSeqEdit database report and the location of the first nucleotide is marked with "insert starts here" and an arrow. The

location of the last nucleotide corresponding to SEQ ID NO:161 is shown on page 11 and is marked with an arrow.

13. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO:162 disclosed in the above-identified application.
14. The amino acid residues of the PRO615 polypeptide (SEQ ID NO:162) encoded by the cDNA (DNA48304) are shown in the GSeqEdit report starting on page 2 and continuing until page 7 of the report.
15. Exhibit A clearly shows that both the full-length DNA48304 sequence and the full-length PRO615 polypeptide sequence disclosed in the above-identified application, as well as the homology of PRO615 to human synaptogyrin were obtained prior to March 3, 1998.
16. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

B. Goddard
Audrey Goddard

9/10/04
Date

Paul J. Godowski, Ph.D.

Date

Austin Gurney, Ph.D.

Date

Margaret Roy, Ph.D.

Date

William I. Wood, Ph.D.

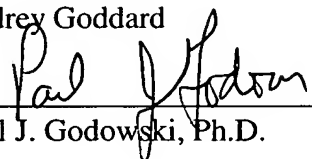
Date

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Audrey Goddard

Date



Paul J. Godowski, Ph.D.

9/09/2001

Date

Austin Gurney, Ph.D.

Date

Margaret Roy, Ph.D.

Date

William I. Wood, Ph.D.

Date

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Audrey Goddard

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Audrey Goddard

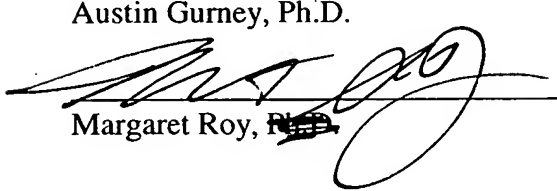
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Paul J. Godowski, Ph.D.

Date

Austin Gurney, Ph.D.

Date



Margaret Roy, Ph.D.

Date

9/16/04

William I. Wood, Ph.D.

Date

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Audrey Goddard

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Paul J. Godowski, Ph.D.


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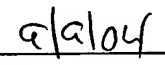
Date

Margaret Roy, Ph.D.

Date



William I. Wood, Ph.D.



Date

>[REDACTED]

>DNA48304 [Full]

>707 Sites [All Sites]

>[REDACTED] DNA48304 brush GSeqEdit

```

rmaI
maeI
sau3AI
mboI/ndeII[dam-]
dpnII[dam-]
dpcI[dam+]
alwI[dam-] sau3AI
taqI
sfuI tsp509I[M.ecoRI-] nlaIV xbaI mboI/ndeII[dam-]
bstBI mwoI haeIII/palI bfaI dpnII[dam-]
bsiCI bglI[M.haeIII-] hpy188II taqI
tfII apoI sfII eaeI bstYI/xhoII dpnI[dam+]
hinfi[M.taqI-] cfrI bamHI[M.mspI-] mnlI
mnli taqI[M.claI-] haeIII/palI alwI[dam-] alwI[dam-] drdI
bsaJI claI/bsp106 eaeI bsrI mspI[M.bamHI-][M.haeIII-] taqI
hpyCH4V bspDI[dam-] cfrI tspRI hpaII mnlI bstYI/xhoII mnlI
1 TGCACCTCGG TTCTATCGAT TCGAATTCGG CCACACTGGC CGGATCCTCT AGAGATCCCT CGACCTCGAC CCACGCGTCC GCGGACGCGT GGGCGGACGC
ACGTGGAGCC AAGATAGCTA AGCTTAAGCC GGTGTGACCG GCCTAGGAGA TCTCTAGGGA GCTGGAGGTG GGTGCGCAGG CGCCTGGCA CCCGCCTGCG
^insert starts here
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```

    eaeI
    mwoI
    fnu4HI/bsoFI
    thai styl
    fnuDII/mvnI
    bstUI[M.hhaI-]
    bsh1236I
    hinPI bsaJI
    hhaI/cfoI
    mwoI
    nlaIV bceAI aciI
    eco0109I/draII haeIII/pali aciI
    bsrBI sau96I[M.haeIII-]
    nlaIII aciI haeIII/pali cfrI
    aciI hpy99I
    mwoI fnu4HI/bsoFI bceAI
    fnu4HI/bsoFI fnu4HI/bsoFI
    aciI bbvI
    101 GTGGGGCGGC GGCAGCGGC GCGACGGCGA CATGGAGAGC GGGGCCCTACG GCGCGGCCAA GCGGGGCGGC TCCTTCGACC TCGGGCGGCTT CCTGACGCAG
    CACCCCGCGC CCGTCGCGGC CGCTGCCGCT GTACCTCTCG CCGCGGATGC CCGCGCGGTT CCGCGCGCGC AGGAAGCTGG AGCCCGCGAA GGAAGCTGTC
    M E S G A Y G A A K A G G S F D L R R F L T Q
    ^MET

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```

mwol
hinPI
hhaI/cfoI
thaI
fnuDII/mvnI
bstUI[M.hhaI-]
bsh1236I
hinPI
hhaI/cfoI
cac8I
bssHII
thaI
fnuDII/mvnI
bstUI[M.hhaI-]
bsh1236I
hinPI
hhaI/cfoI
cac8I bceAI
bssHII
bspMI
aciI
201 CCGCAGGTGG TGGCGGGCGC CGTGTGCTTG GTCTTCGCCT TGATCGTGTTCCTCTGCATC TATGGTGAGG GCTACAGCAA TGCCCACGAG TCTAAGCAGA
GGCGTCCACC ACCGGGCGCG GCACACGAAC CAGAAGCGGA ACTAGCACAA GAGGACGTAG ATACCACTCC CGATGTCGTT ACGGGTGCTC AGATTGCTCT
24 P Q V V A R A V C L V F A L I V F S C I Y G E G Y S N A H E S K Q M

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pleI
mlyI
hinfi
bsrDI bssSI ddeI
sfiI bsrDI bssSI ddeI
mnlI
hphI
hpyCH4V
sfaNI
dpnII[dam-]
dpnI[dam+]
24 P Q V V A R A V C L V F A L I V F S C I Y G E G Y S N A H E S K Q M

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mvaI
ecorII[dcn-]
dsaV[dcn-]
bstNI
bssKI[dcn-]
sau3AI
mboI/ndeII[dam-]
dnpII[dam-]
dnpI[dam+]
tspRI
acII
csp6I
tspRI
acII
csp6I
tsp45I
maeIII
earI/ksp632I
sau96I
hphI
bspMI
mboII
aluI
avaII
hphI
bspCNI
hpy188III
401 GTATTTCCTCC CAGATCAGCA ACGCCACTGA CCGCAAGTAC CTGGTCATG GTGACCTGCT CTTCTCAGCT CTCTGGACCT TCCTGTGGTT TGTGGTTTC
CATAAAGGG GTCTAGTCGT TCGGTGACT GCGGTTCATG GACCAAGTAC CACTGGACGA GAAGAGTGA GAGACCTGGA AGGACACCAA ACAACCAAAG
91 Y F P Q I S N A T D R K Y L V I G D L L F S A L W T F L W F V G F

pleI
haeIII/palI
sau96I[M.haeIII-]
fnu4HI/bsoFI
tseI
pflMI
hphI
hphI
tsp45I
maeIII
bsrI
bsrI
tspRI
maeIII
mnlI
bslI
tspRI
maeIII
mnlI
hinfI
mnlI
hphI
eco57I
mboI
501 TGCTTCCTCA CCAACCAAGT GGCAGTCACC AACCCGAAG ACCTGCTGCT GGGGGCCGAC TCTGTGAGG CAGCCATCAC CTTCAGCTTC TTTTCCATCT
ACGAAGGAGT GGTGGTGCAC CCGTCAGTGG TTGGGCTTCC TGCACGACCA CCCCCGGCTG AGACACTCC GTCCGGTAGT GAAGTCGAAG AAAAGGTAGA
124 C F L T N Q W A V T N P K D V L V G A D S V R A A I T F S F F S I F

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    nlaIV
    mspI
    mroI
    hpy188III
    bspMII
    bspEI
    hincII/hindII
    avaII[M.hpaII-]
    hpy188III
    tail
    bsaWI
    fokI
    maeII/hpyCH4IV
    hpaII
    tspR
    btsI
    bstF5I
    tsp509I
    bslI
    accIII
    btsI
    601 TCTCCTGGGG TGTGCTGGCC TCCCTGGCCT ACCAGCGCTA CAAGGCTGGC GTGGACGACT TCATCCAGAA TTACGTTGAC CCCACTCCGG ACCCCAACAC
    AGAGGACCCC ACACGACCGG AGGACCGGA TGCTCGCAT GTTCCGACCG CACTGCTGA AGTAGGCTT AATGCACACTG GGTGAGGCC TGGGGTTGTG
158 S W G V L A S L A Y Q R Y K A G V D D F I Q N Y V D P T P D P N T

scrFI[dcM-]
    bsmAI
    bsaI
    acII
    thal
    fnuDII/mvnI
    bslI
    bstUI
    mnlI
    acII
    rs
    mnlI
    bsaJI
    bsh1236I
    fnu4HI/bsaFI
    cs
    701 TGCTAGGCC TCCTACCCAG GTGCATCTGT GGACAACCTAC CAACAGCCAC CCTTCACCCA GAACGGGAG ACCACCGAG GCTACCAGCC GCCCCTGTG
    ACGGATCGG AGGATGGTC CACGTAGACA CCTGTTGATG GTTGTGCGTG GGAAGTGGT CTTGCGCTC TGGTGGCTCC CGATGGTCG CGGGGGACAC
191 A Y A S Y P G A S V D N Y Q Q P P F T Q N A E T T E G Y Q P P P V

```

sau96I[M.haeIII-]
haeIII/palI
sau96I[M.haeIII-] scrFI[dcM-]
pspOMI/bsp120I pspGI
nlaIV mvaI
eco0109I/draII ecoRII[dcM-]
bsp1286[M.haeIII-]
bmyI dsav[dcM-]
banII[M.haeIII-] bstNI
apaI bssKI[dcM-]
eco0109I/draII apyI[dcM+]
bsmFI mnII mnII mnII xcmI
bspcNI aciI bsmFI mnII mnII mnII bsaJI xcmI
801 TACTGAGTGG CGGTAGCGT GGAAGGGG ACAGAGAGG CCTCCCTC TGCCCTGGAC TTTCCTATCA GCCTCCTGGA ACTGCCAGCC CCTCTCTTTC
ATGACTCACC GCCAATCGCA CCTTCCCC TGCTCTCCC GGGAGGGGAG ACGGACCTG AAAGGTAGT CGGAGGACCT TGACGGTCGG GGAGAGAAAG

224 Y 0

scrFI[dcM-]
pspGI
mvaI
ecoRII[dcM-]
dsav[dcM-]
bstNI
mnII
bsbKI[dcM-]
bslI[dcM-] mwOI
apyI[dcM+] cac8I
bmyI mnII eco57
901 ACCTGTTCCTA TCCTGTGCAG CTGACACACA GCTAAGAGC CTCATAGCCT GCGGGGGCT GGCAGAGCCA CACCCCAAGT GCCTGTGCCC AGAGGGCTTC
TGGACAAGGT AGGACACGTC GACTGTGTGT CGATTCTCTG GAGTATCGGA CCGCCCCCGA CGCTCTCGGT GTGGGGTTCA CGGACACGGG TCTCCCCGAAAG

scrFI[dcn-]

pspGI

mvaI

ecoRII[dcn-]

dsaV[dcn-]

bstNI

bssKI[dcn-]

bsaJI

bpmI/gsuI[dcn-]

bsrBI mnlI bspI286

aciI bseRI bmyI

fnu4HI/bsaFI apyI[dcn+]

rmaI

maeI

bfaI

aluI

tspRI

btsI

sfcI

pstI rmaI

maeI

bfaI

ddeI

bspCNI aciI hpyCH4V

maeI

1001 AGTCAGCCGC TCACCTCCTCC AGGGCACTTT TAGGAAAGGG TTTTGTAGCTA GTGTTTTTCC TCGCTTTTAA TGACCTCAGC CCCGCCCTGCA GTGGCTAGAA

TCAGTCGGCG AGTGAGGAGG TCCCGTGAAA ATCCCTTTCC AAAAAATCGAT CACAAAAAGG AGCGAAAAAT ACTGGAGTCG GGGCGGACGT CACCGATCTT


```

scrFI[dcM-]
pspGI
mvaI
ecoRII[dcM-]
mspAII/nspBII dsav[dcM-]
tseI sau96I[dcM-]
fnu4HI/bsoFI bstNI
bbvI nlaIV avaII[dcM-][M.hpaII-] ddeI
haeIII/paII
sau96I[M.haeIII-] hpyCH4V mspI bssKI[dcM-] ecoNI
nlaIV bspMI bsgI aciI hpaII apyI[dcM+] bsII bspCNI
1201 CGTGGGGCC ATCACACCTG CCCTGTGCAG CGGAGCCGGA CCAGGCTCTT GTGTCTCTAC TCAGGTTTGC TTCCCTCTGTG CCCACTGCTG TATGATCTGG
GCACCCCGG TAGTGTGGAC GGGACACGTC GCCTCGGCCT GTCCGAGAA CACAGGAGTG AGTCCAAAG AAGGGGACAC GGGTGACGAC ATACTAGACC

nl
sau3AI
mboI/nde
dpnII[da
dpnI[dam
tspRI
bspl286
bmyI btsI
1201 CGTGGGGCC ATCACACCTG CCCTGTGCAG CGGAGCCGGA CCAGGCTCTT GTGTCTCTAC TCAGGTTTGC TTCCCTCTGTG CCCACTGCTG TATGATCTGG
GCACCCCGG TAGTGTGGAC GGGACACGTC GCCTCGGCCT GTCCGAGAA CACAGGAGTG AGTCCAAAG AAGGGGACAC GGGTGACGAC ATACTAGACC

tseI
fnu4HI
scrFI[dcM-]
pspGI
mvaI
ecoRII[dcM]
dsav[dcM-]
bstNI
bssKI[dcM-]
apyI[dcM+]
bsaJI
bsII mspI
draIII hpaII mnII
haeIII/paII cfr10I/bsrFI bbvI bsaJI
sau96I[M.haeIII-] haeIII/paII mnII
1301 GGGCCACCAC CCTGTGCCGG TGGCCTCTGG GCTGCCTCCC GTGGTGTGAG GGGGGGGCTG GTGCTCATGG CACTTCTCTCC TTGCTCCCAC CCCTGGCAGC
CCCGTGGTG GGACACGGCC ACCGGAGACC CGACGGAGG CACCACACTC CCGCCCCGAC CACGAGTACC GTGAAGGAGG AACGAGGGTG GGGACCGTGC

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scrFI[dcm-]
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 mvaI
 nlaIII
 tth
 ple
 pfl
 mly
 bspI286
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 nlaIV btgI/bstDSI hin
 banI bsaJI alw26
 GGAGGGCAGG
 GGAGGGCAGG
 CCTCCCGTCC
 CCGAGGGTCT

scrFI[dcm-]

pspGI

mvaI

ecoRII[dcm-]

dsaV[dcm-]

bstNI

mwoI

haeIII/palI

mspI[M.haeIII-]

scrFI[M.hpaII-]

nciI bssKI[dcm-]

dsaV bsaJI sfaNI

bssKI foki

bslI apyI[dcm+]

sfaNI hpaII bstF5I

psII

1501 CTCTGTCTGT GCCGAGTGTA TTATAAAATC GTGGGGGAGA TGCCCGGCCT GGATGCTGT TTGGAGACGG AATAATGTT TTCTCATTCA AAGAAAAAAA
 GAGACAGACA CGGCTCACAT AATAATTTAG CACCCCTCTCT ACGGGCCGGA CCTACGACA AACCTCTGCC TTATTACAA AAGAGTAAGT TTCCTTTTTT

```

    thai
    fnu4HI/bsoFI
    haeIII/palI
    mcrI    rnaI
    eagI/xmaIII/ecI XI
    eaeI    maeI
    cfrI    pleI
    bsiEI   mlyI    taqI
    notI fnuDII/mvni   sali
    fnu4HI/bsoFI bfaI hincII/hindII[M.taqI-]
    aciI bstUI xbaI accI[M.taqI-]
    thai aciI hinfI pleI
    fnuDII/mvni hpy188III
    bstUI bsh1236I mlyI
    bsh1236I drdI hinfI[M.taqI-]
    1601 AAAAAAAAAA AACGGGGCC GCGACTCTAG AGTCGACCTG
    TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
    ^PRK follows

```

> length: 1640

```

accI(GTMKAC):          393 1632
accIII(TCCGGA):       79 81 93 106 109 115 118 139 153 162 166 182 201 317 335 431 765 789
aciI(CCGC):           810 952 1007 1082 1170 1230 1352 1615 1619
afeI(AGCGCT):         634
aflIII(ACRYGT):       73 85 97 397
aluI(AGCT):           467 585 919 930 1046 1137 1428

```

| | |
|--|---|
| alw26I (CAGNNNCTG) : | 1497 |
| alwI (GGATCNNNN) : | 42 43 54 |
| alwNI (CAGNNNCTG) : | 1497 |
| apaI (GGGCC) : | 838 |
| apoI (RAATTY) : | 23 |
| apyI (CCWGG) : | 368 440 604 623 717 854 875 948 1019 1241 1392 1466 1548 |
| asphi (GWGCWC) : | 1361 |
| aspi (GACNNNGTC) : | 1499 |
| avaI (CYCGRG) : | 1150 |
| avaII (GGWCC) : | 475 689 1238 |
| bamHI (GGATCC) : | 42 |
| banI (GGYRCC) : | 1108 1481 |
| banII (GRGCYC) : | 838 |
| bbsI (GAAGACNNNNNN) : | 231 |
| bbvI (GCAGC) : | 112 197 570 917 1227 1331 1396 |
| bceAI (ACGGCNNNNNNNNNN) : | 124 148 219 1160 |
| bcgI (NNNNNNNNNNCGANNNNNTGCNNNNNNNNNNNN) : | 343 535 |
| bfaI (CTAG) : | 49 1048 1095 1627 |
| bgII (GCCNNNNNGGC) : | 30 334 363 618 987 |
| bmyI (GDGCHC) : | 838 985 1022 1109 1278 1361 1482 |
| bpmI (CTGGAG) : | 1017 |
| bpuAI (GAAGACNNNNNNNN) : | 231 |
| bsaI (GGTCTCNNNNNN) : | 768 |
| bsaJI (CCNNGG) : | 5 79 157 373 604 622 716 775 853 1019 1144 1150 1161 1339 1391 1466 |
| | 1487 1548 |
| bsaWI (WCCGGW) : | 686 |
| bseRI (GAGGAGNNNNNNNNNN) : | 1014 |
| bsgI (GTGCAG) : | 915 1225 |
| bsh1236I (CCCG) : | 74 80 86 98 152 214 216 398 764 1614 1620 |
| bsiCI (TTCGAA) : | 20 |

| | | |
|--------------------------------|----------------------------------|------------------------------------|
| -bsiEI (CGRYCG): | 1616 | |
| bsiHKAI (GWGCWC): | 1361 | |
| bsli (CCNNNNNNNGG): | 317 368 478 511 680 758 948 1144 | 1145 1150 1255 1310 1386 1466 1543 |
| bsmAI (GTCTC): | 768 1564 | |
| bsmAI (GTCTC): | 768 1564 | |
| bsmBI (CGTCTCNNNN): | 1564 | |
| bsmFI (GGGACNNNNNNNNNNNNNNNN): | 828 | |
| bsoFI (GCNGC): | 106 109 112 115 118 153 166 182 | 197 200 334 570 788 917 1006 1169 |
| | 1227 1331 1396 1615 1618 | |
| | 15 | |
| bsp106 (ATCGAT): | 838 | |
| bsp120I (GGGCC): | 838 985 1022 1109 1278 1361 1482 | |
| bsp1286 (GDGCHC): | 464 803 1075 1134 1260 | |
| bspCNI (CTCAGNNNNNNNNNN): | 15 | |
| bspDI (ATCGAT): | 686 | |
| bspEI (TCCGGA): | 178 203 454 1105 1216 | |
| bspMI (ACCTGC): | 686 | |
| bspMII (TCCGGA): | 137 1007 | |
| bsrBI (GAGCGG): | 277 | |
| bsrDI (GCAATGNN): | 1316 | |
| bsrFI (RCCGGY): | 35 515 | |
| bsrI (ACTGGN): | 213 215 | |
| bssHII (GCGCGC): | 368 440 604 623 717 854 875 948 | 1019 1145 1150 1151 1241 1392 1466 |
| bssKI (CCNGG): | 1543 1548 | |
| | 285 1199 | |
| | 20 | |
| bssSI (CTCGTG): | 79 1161 1339 1487 | |
| bstBI (TTCGAA): | 450 | |
| bstDSI (CCRYGG): | 326 662 909 1552 | |
| bstEII (GGTNACC): | 368 440 604 623 717 854 875 948 | 1019 1241 1392 1466 1548 |
| bstF5I (GGATG): | | |
| bstNI (CCWGG): | | |

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|----------------------|--|
| bstUI (CGCG): | 74 80 86 98 152 214 216 398 764 1614 1620 |
| bstYI (RGATCY): | 42 53 |
| btgI (CCRYGG): | 79 1161 1339 1487 |
| btrI (CACGTC): | 540 |
| btsI (GCAGTGNN): | 343 698 1088 1283 |
| cac8I (GCNNGC): | 162 213 215 330 359 614 645 884 958 1084 1101 |
| cfoI (GCGC): | 151 185 213 215 217 635 |
| cfr10I (RCCGGY): | 1316 |
| cfrI (YGGCCR): | 28 37 154 1616 |
| claiI (ATCGAT): | 15 |
| csp6I (GTAC): | 302 437 800 |
| ddeI (CTNAG): | 292 464 803 932 1075 1134 1260 1457 |
| dpnI (GATC): | 43 54 242 413 1294 |
| dpnII (GATC): | 43 54 242 413 1294 |
| draII (RGNCCY): | 141 837 838 |
| draIII (CACNNGTG): | 1308 |
| drdI (GACNNNNNGTC): | 68 1623 |
| dsaI (CCRYGG): | 79 1161 1339 1487 |
| dsaV (CCNGG): | 368 440 604 623 717 854 875 948 1019 1145 1150 1151 1241 1392 1466 |
| | 1543 1548 |
| eaeI (YGGCCR): | 28 37 154 1616 |
| eagI (CGGCCG): | 1616 |
| earI (CTCTTCNNNN): | 459 |
| eciI (GGCGGA): | 92 |
| ecXI (CGGCCG): | 1616 |
| eco47III (AGCGCT): | 634 |
| eco57I (CTGAAG): | 581 997 |
| econI (CCTNNNNNAGG): | 1255 |
| ecoO109I (RGNCCY): | 141 837 838 |
| ecoRI (GAATTC): | 23 |

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|-----------------------|--|
| - ecorII (CCWGG): | 368 440 604 623 717 854 875 948 1019 1241-1392 1466 1548 |
| esp3I (CGTCTC): | 1564 |
| fnu4HI (GCNGC): | 106 109 112 115 118 153 166 182 197 200 334 570 788 917 1006 1169 |
| | 1227 1331 1396 1615 1618 |
| fnuDII (CGCG): | 74 80 86 98 152 214 216 398 764 1614 1620 |
| fokI (GGATG): | 326 662 909 1552 |
| gsuI (CTGGAG): | 1017 |
| haeII (RGGCY): | 184 634 |
| haeIII (GGCC): | 29 38 143 155 362 371 377 554 617 626 839 1148 1159 1207 1302 1322 |
| | 1546 1617 |
| | 75 84 96 194 396 |
| hgaI (GACGC): | 1361 |
| hgiAI (GWGCWC): | 151 185 213 215 217 635 |
| hhaI (GCGC): | 151 185 213 215 217 635 |
| hinPI (GCGC): | 393 675 1632 |
| hincII (GTYRAC): | 393 675 1632 |
| hindII (GTYRAC): | 18 288 558 1197 1499 1623 1630 |
| - hinfI (GANTC): | 40 687 1146 1151 1236 1317 1544 |
| hpaII (CCGG): | 264 450 508 526 577 754 899 |
| hphI (GGTGA): | 48 190 472 664 686 1626 |
| hpy188III (TCNNGA): | 122 395 |
| hpy99I (CGWCG): | 541 673 |
| hpyCH4IV (ACGT): | 1 255 722 916 1087 1226 1446 |
| hpyCH4V (TGCA): | 459 |
| ksp632I (CTCTTCNNNN): | 79 |
| kspI (CCCGCG): | 49 1048 1095 1627 |
| maeI (CTAG): | 541 673 |
| maeII (ACGT): | 451 525 1453 |
| maeIII (GTNAC): | 43 54 242 413 1294 |
| mboI (GATC): | 232 382 460 598 |
| mboII (GAAGA): | |

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|-----------------------|--|
| mcrI (CGRYCG) : | 1616 |
| mluI (ACGGGT) : | 73 85 97 397 |
| mlyI (GAGTCNNNNN) : | 288 558 1197 1499 1623 1630 |
| mnlI (CCTC) : | 5 46 58 64 267 324 373 506 566 619 709 777 836 842 847 872 891 940 |
| | 992 1016 1059 1074 1133 1255 1324 1335 1348 1376 1472 |
| mroI (TCCGGA) : | 686 |
| mseI (TTAA) : | 1067 |
| mslI (CAYNNNNRTG) : | 350 |
| mspAII (CMGCKG) : | 79 113 918 1228 |
| mspI (CCGG) : | 40 687 1146 1151 1236 1317 1544 |
| mvaI (CCWGG) : | 368 440 604 623 717 854 875 948 1019 1241 1392 1466 1548 |
| mvnI (CCGG) : | 74 80 86 98 152 214 216 398 764 1614 1620 |
| mwol (GCNNNNNNNGC) : | 30 106 109 112 118 144 153 217 334 363 618 958 987 1079 1160 1182 |
| | 1547 |
| nciI (CCSGG) : | 1145 1150 1151 1543 |
| ncol (CCATGG) : | 1487 |
| ndeII (GATC) : | 43 54 242 413 1294 |
| nlaIII (CATG) : | 131 1114 1366 1488 |
| nlaIV (GGNNCC) : | 42 141 168 552 689 838 936 1108 1166 1205 1232 1300 1481 1491 |
| notI (GCGGCCGC) : | 1615 |
| nspBII (CMGCKG) : | 79 113 918 1228 |
| pali (GGCC) : | 29 38 143 155 362 371 377 554 617 626 839 1148 1159 1207 1302 1322 |
| | 1546 1617 |
| | 1499 |
| pflFI (GACNNNGTC) : | 511 |
| pflMI (CCANNNNNTGG) : | 288 558 1197 1499 1623 1630 |
| pleI (GAGTCNNNN) : | 1521 |
| psiI (TTATAA) : | 1150 |
| pspAI (CCCGGG) : | 368 440 604 623 717 854 875 948 1019 1241 1392 1466 1548 |
| pspGI (CCWGG) : | 838 |
| pspOMI (GGGCCC) : | |

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|-----------------------|--|
| -pstI (CTGCAG): | 1086 1445 |
| -pvuII (CAGCTG): | 918 |
| rmaI (CTAG): | 49 1048 1095 1627 |
| rsaI (GTAC): | 302 437 800 |
| sacII (CCGCGG): | 79 |
| sali (GTCGAC): | 393 1632 |
| sapI (GCTCTTCNNNN): | 458 |
| sau3AI (GATC): | 43 54 242 413 1294 |
| sau96I (GGNCC): | 142 475 553 689 838 839 1148 1206 1238 1301 |
| scrFI (CCNGG): | 368 440 604 623 717 854 875 948 1019 1145 1150 1151 1241 1392 1466 |
| | 1543 1548 |
| sexAI (ACCWGGT): | 439 |
| sfanI (GCATC): | 256 327 723 1539 1553 |
| sfcI (CTRYAG): | 272 1086 1445 |
| sfiI (GGCCNNNNNGGCC): | 29 362 617 |
| sfuI (TTCGAA): | 20 |
| smaI (CCCGGG): | 1150 |
| sspI (AATATT): | 1439 |
| sstII (CCGCGG): | 79 |
| styI (CCWWGG): | 157 1487 |
| taII (ACGT): | 541 673 |
| taqI (TCGA): | 16 21 60 66 175 394 1633 |
| tfiI (GAWTC): | 18 |
| thai (CGCG): | 74 80 86 98 152 214 216 398 764 1614 1620 |
| tru9I (TTAA): | 1067 |
| tseI (GCGC): | 112 197 570 917 1227 1331 1396 |
| tsp45I (GTSAC): | 451 525 |
| tsp509I (AATT): | 24 669 |
| tspRI (NNCAGTGNN): | 34 344 425 516 698 1089 1283 |
| tth111I (GACNNNGTC): | 1499 |

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|-------------------------|---------|
| xbaI (TCTAGA) : | 48 1626 |
| xcmI (CCANNNNNNNNTGG) : | 349 865 |
| xhoII (RGATCY) : | 42 53 |
| xmaI (CCCGGG) : | 1150 |
| xmaIII (CGGCCG) : | 1616 |

not found:

aatII (GACGTc), acc65I (GGTACC), acLI (AAGCTT), acyI (GRCGYC), aflII (CTTAAG), ageI (ACCGGT), ahaII (GRCGYC), ahaIII (TTTAAA),
ahdI (GACNNNNNGTC), alw44I (GTGCAC), apaLI (GTGCAC), asci (GGCGGCC), aseI (ATTAAT), asnI (ATTAAT), asp700 (GAANNNTTC),
asp718 (GGTÀCC), avaIII (ATGCAT), avII (TGCGCA), avrII (CCTAGG), bæI (NNNNNNNNNNNACNNNGTAYCNNNNNNNNNN), balI (TGCCCA),
bbrPI (CACGTG), bciVI (GTATCC), bcLI (TGATCA), bfrBI (ATGCAT), bfrI (CTTAAG), bgII (àGATCT), blnI (CCTAGG), blpI (GCTNAGC),
bpul102I (GCTNAGC), bsalI (YACGTR), bsalBI (GATNNNATC), bsalHI (GRCGYC), bsaxI (NNNNNNNNNNNACNNNNNNCTCCNNNNNNNNNN),
bsiWI (CGTAGC), bsmI (GAATGcn), bsp1407I (TGTACA), bspCI (CGATCG), bspHI (TCATGA), bsrGI (TGTACA), bst1107I (GTATAC),
bst4CI (ACNGT), bstAPI (GCANNNNTGG), bstXI (CCANNNNTGG), bstZ17I (GTATAC), bsu36I (CCTNAGG), celII (GCTNAGC), cpoI (CGGWCCG),
cspI (CGGWCCG), draI (TTTTAA), eam1105I (GACNNNNNGTC), ecl136I (GAGCTC), eco72I (CACGTG), eco81I (CCTNAGG), ecoRV (GATATC),
eheI (GGCGCC), espI (GCTNAGC), fseI (GGCGGCC), fpsI (TGCGCA), hindIII (AAGCTT), hinLI (GRCGYC), hpaI (GTAAAC), hpy188I (TCNGA),
hpyCH4III (ACNGT), kasI (GGCGCC), kpnI (GGTACC), mamI (GATNNNNATC), mfeI (CAATTG), mscI (TGGCCA), mstII (CCTNAGG), munI (CAATTG),
naeI (GCCGGC), narI (GGCGCC), ndeI (CATATG), ngoMI (GCCGGC), nheI (GCTAGC), nruI (TCGCGA), nsiI (ATGCAT), ñspHI (RCATGY),
nspI (RCATGY), pacI (TTAATTAA), paeR7I (CTCGAG), pciI (ACATGT), pmeI (GTTTAAAC), pmLI (CACGTG), ppulOI (ATGCAT), ppmI (RGGWCCY),
pshAI (GACNNNNNGTC), psp1406I (AAGCTT), pvuI (CGATCG), rcaI (TCATGA), rsrII (CGGWCCG), sacI (GAGCTC), sandI (GGGWCCC),
sauI (CCTNAGG), sbfI (CCTGCAGG), scaI (ACTACT), sceI (TAGGGATAACAGGTAAT), sgfi (GCGATCGC), sgrAI (CRCCGGYG), smLI (CTYRAG),
snaBI (TACGTA), snoI (GTGCAC), snoI (GTGCAC), speI (ACTAGT), sphI (GCATGC), splI (CGTACG), sfrI (GCCGGGGC), sse8387I (CCTGCAGG),
sstI (GAGCTC), stuI (AGGCCT), swaI (ATTTAAAT), tliI (CTCGAG), vspI (ATTAAT), xhoI (CTCGAG), xmnI (GAANNNTTC)

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